We Claim:

1. A pair of polymerase chain reaction primers for amplifying a 16S rRNA gene of eubacteria selected from the group consisting of :
   PEU 7 and PEU 8 (SEQ ID NO 1 and 2); and
   PEU 4 and PEU 5 (SEQ ID NO: 3 and 4).
2. A method of performing polymerase chain reaction comprising:

digesting reagents for polymerase chain reaction with a restriction endonuclease, wherein the reagents comprise Taq DNA polymerase, deoxynucleotide triphosphates, reaction buffer, and primers, wherein the restriction endonuclease does not cleave said primers and said primers have no recognition sites for the restriction endonuclease;

inactivating said restriction endonuclease but not said Taq DNA polymerase;

mixing test sample and the reagents for polymerase chain reaction to form a mixture;

subjecting the mixture to conditions such that any templates present in the test sample which hybridize to both primers are amplified;

detecting amplification product, wherein a detected amplification product indicates the presence of template which hybridizes to both primers in the test sample.

3. The method of claim 2 wherein the restriction endonuclease is AluI.
4. The method of claim 2 wherein the step of inactivating comprises heating to a temperature which inactivates the restriction endonuclease but not the Taq DNA polymerase.
5. The method of claim 2 wherein the test sample is a treated blood sample.
6. The method of claim 5 wherein the blood sample is from a patient suspected of systemic bacteremia.
7. The method of claim 2 wherein the primers are PEU7 and PEU8.
8. The method of claim 3 wherein the step of inactivating is performed at about 65° C for about 20 minutes.
9. The method of claim 2 wherein the step of detection employs an agarose gel.

10. The method of claim 9 wherein amplification product is labeled with ethidium bromide and visualized under ultraviolet light.
11. The method of claim 5 wherein the blood sample was treated to extract DNA therefrom.
12. The method of claim 2 wherein the sample is urine.
13. The method of claim 2 wherein the sample is cerebrospinal fluid.
14. The method of claim 2 wherein the primers hybridize to at least 10 eubacterial species' DNA in regions which are highly conserved.
15. The method of claim 2 wherein the primers hybridize to 16S RNA genes.
16. The method of claim 2 further comprising the step of:

identifying a bacterial species as a source of the templates by sequencing the amplification product.

17. The method of claim 2 further comprising the step of:

identifying a bacterial species as a source of the templates by restriction endonuclease digestion of the amplification product and determining sizes of products of said digestion.

18. The method of claim 2 further comprising the step of:

identifying a bacterial species as a source of the templates by amplification of the amplification product using primers which hybridize to a single eubacterial species 16S RNA.

19. The method of claim 2 further comprising the step of:

identifying a bacterial species as a source of the templates by amplification of the templates in the test sample using primers which hybridize to a single eubacterial species 16S RNA.

20. The method of claim 2 wherein the Taq DNA polymerase is not active under the conditions used for the step of digesting.
21. The method of claim 2 wherein the amplified product comprises at least one recognition site for the restriction endonuclease.
22. The method of claim 2 wherein the amplified product comprises at least two recognition sites for the restriction endonuclease.

23. A method of performing polymerase chain reaction comprising:

digesting reagents for polymerase chain reaction with AluI restriction endonuclease, wherein the reagents comprise Taq DNA polymerase, deoxynucleotide triphosphates, reaction buffer, and a pair of primers selected from the group consisting of PEU7 and PEU 8 (SEQ ID NO: 1 and 2); and PEU 4 and 5 (SEQ ID NO: 3 and 4);

inactivating said AluI restriction endonuclease by heating said reagents to a temperature which inactivates AluI but does not inactivate Taq DNA polymerase;

mixing a test sample of DNA isolated from a patient's blood sample and the reagents for polymerase chain reaction to form a mixture;

subjecting the mixture to conditions such that any templates present in the test sample which hybridize to both primers are amplified;

detecting an amplification product of 416 or 811 basepairs, wherein a detected amplification product indicates the presence of template which hybridizes to both primers in the patient's blood, which indicates bacteremia in the patient.

24. A kit for detecting bacteremia in a patient sample, comprising:

a pair of primers which hybridize to opposite strands of 16S RNA of at least 10 eubacterial species;

a restriction endonuclease which has a four base pair recognition site; wherein the recognition site does not occur in either of the primers.

25. The kit of claim 19 further comprising:

deoxyribonucleotides, Taq DNA polymerase, and buffer.

26. The kit of claim 19 wherein the primer sequence has been designed to eliminate a recognition site for the restriction enzyme present in said 16S RNA gene.

27. A pair of primers which hybridize to opposite strands of 16S RNA genes of at least 10 eubacterial species at conserved regions, wherein said primers prime synthesis of an amplification product comprising a non-conserved region of said 16S RNA which is distinctive for each of said at least 10 eubacterial species.

28. The pair of primers of claim 24 wherein said primers prime synthesis of an amplification product in each of said at least 10 eubacterial species which contains at least one recognition site for a restriction endonuclease which is not present in said primers.
29. The pair of primers of claim 24 wherein the non-conserved region in the eubacterial species other than *Chlamydia trachomatis* comprises at least 10 base pair differences with respect to the sequence amplified with said primers using *Chlamydia trachomatis* 16S RNA gene (SEQ ID NO: 5) as a template.
30. The pair of primers of claim 24 wherein the non-conserved region in the eubacterial species other than *Chlamydia trachomatis* comprises at least 20 base pair differences with respect to the sequence amplified with said primers using *Chlamydia trachomatis* 16S RNA gene (SEQ ID NO: 5) as a template.
31. The pair of primers of claim 24 wherein the conserved regions comprise at least 18 contiguous base pairs which are at least 80% identical among said 10 eubacterial species.
32. The pair of primers of claim 24 wherein the conserved regions comprises at least 18 contiguous base pairs which are at least 80% identical to a pair of primers selected from the group consisting of: PEU7 and PEU 8 (SEQ ID NO: 1 and 2), and PEU 4 and 5 (SEQ ID NO: 3 and 4).